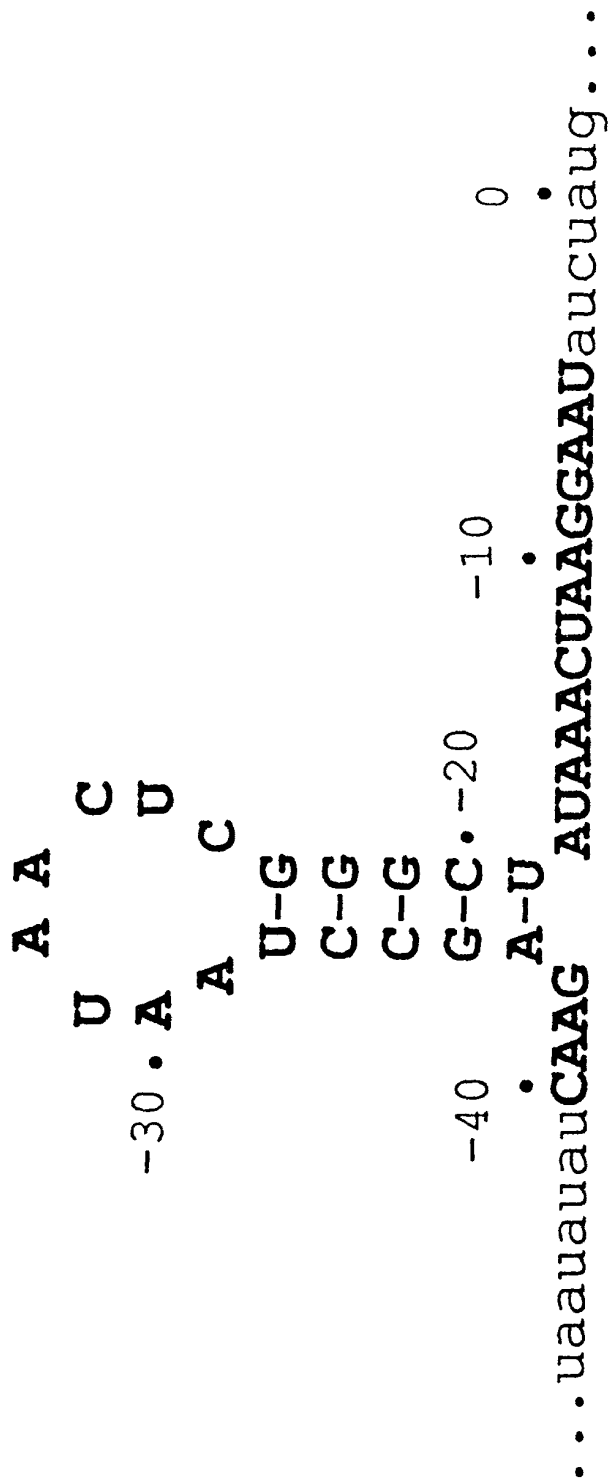


FIG. I



SEQ. I.D. NO. 345

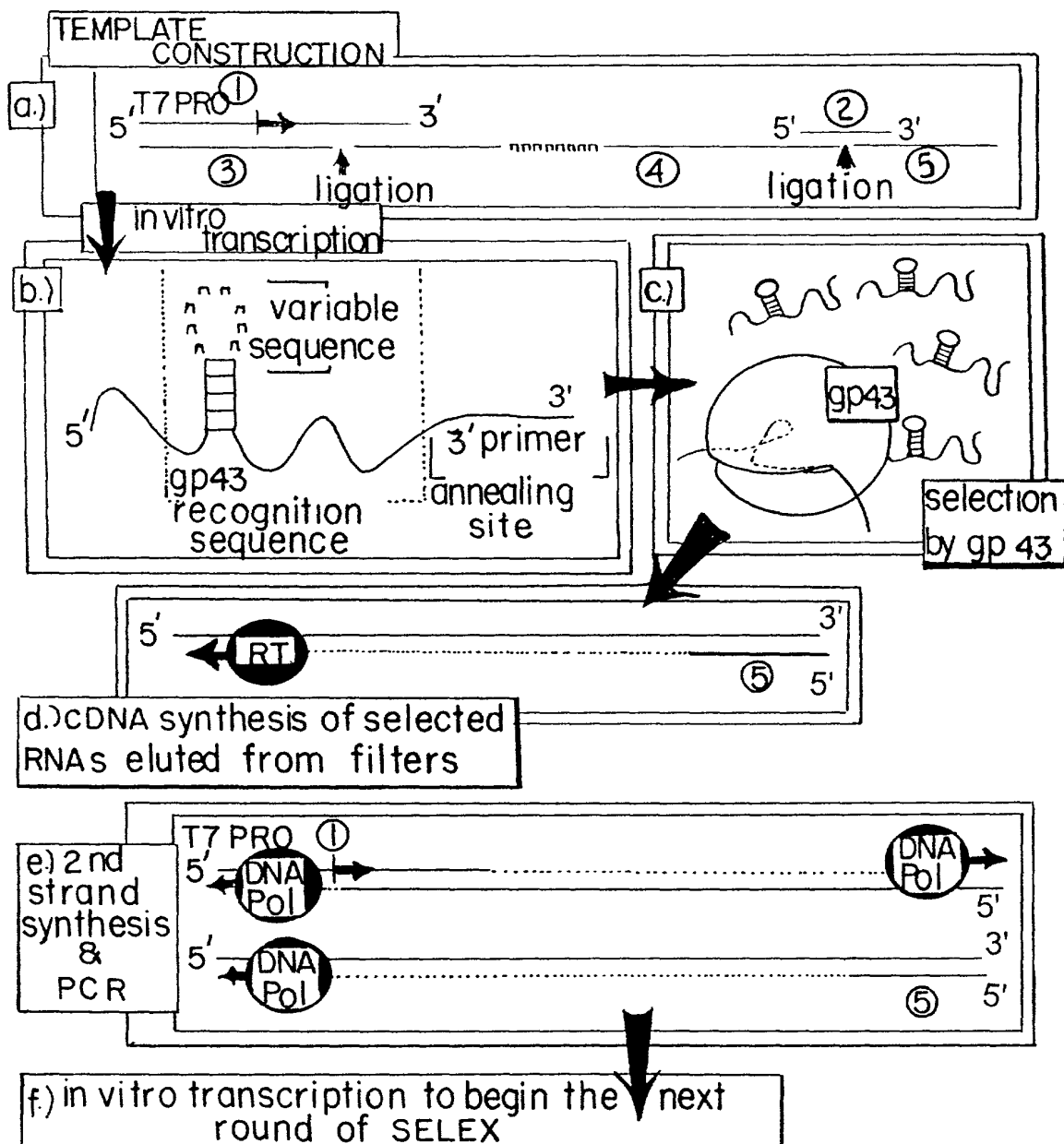


FIG.2

FIG. 3

SELECTION CYCLE:

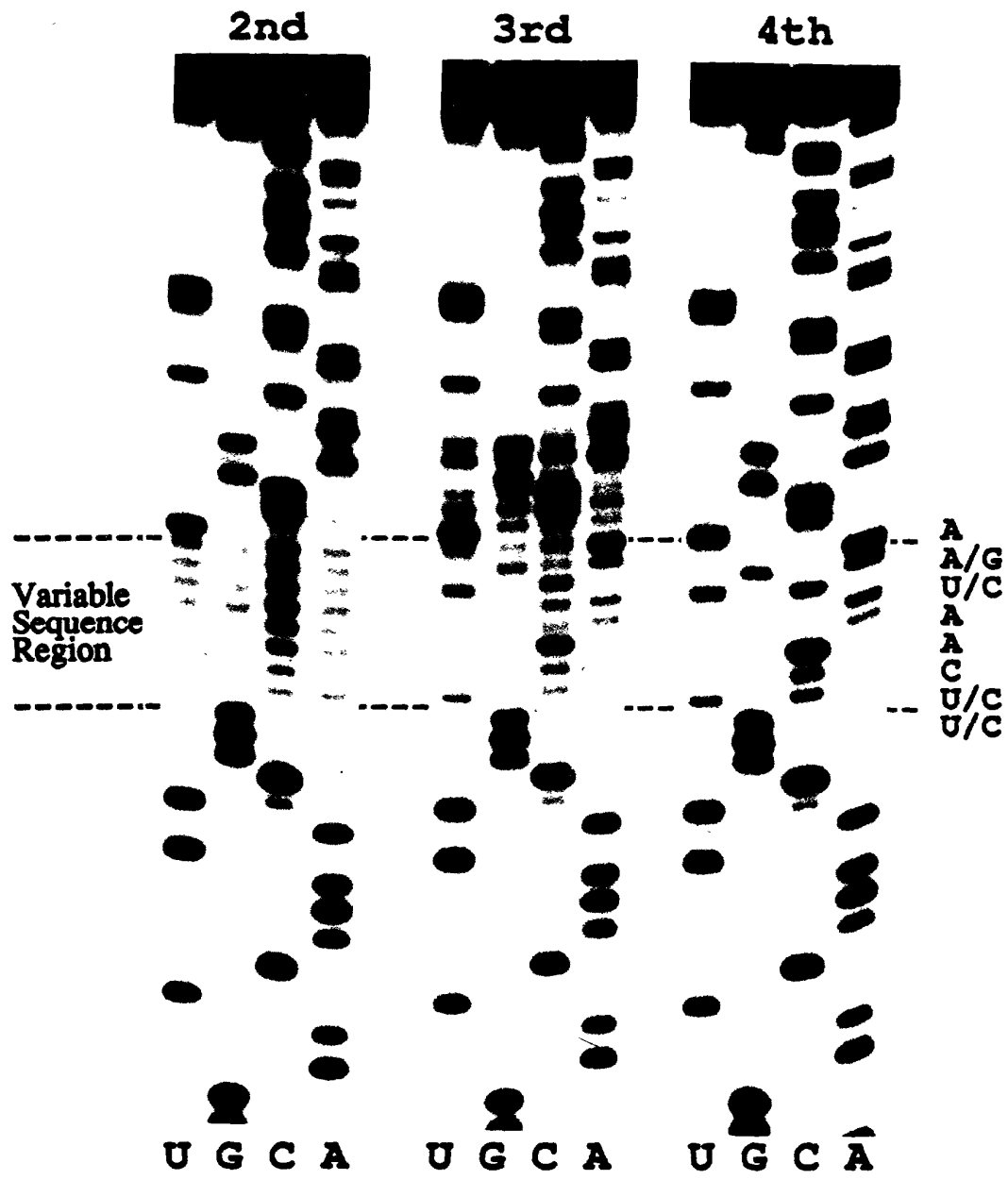


FIG. 4

EXPERIMENT:

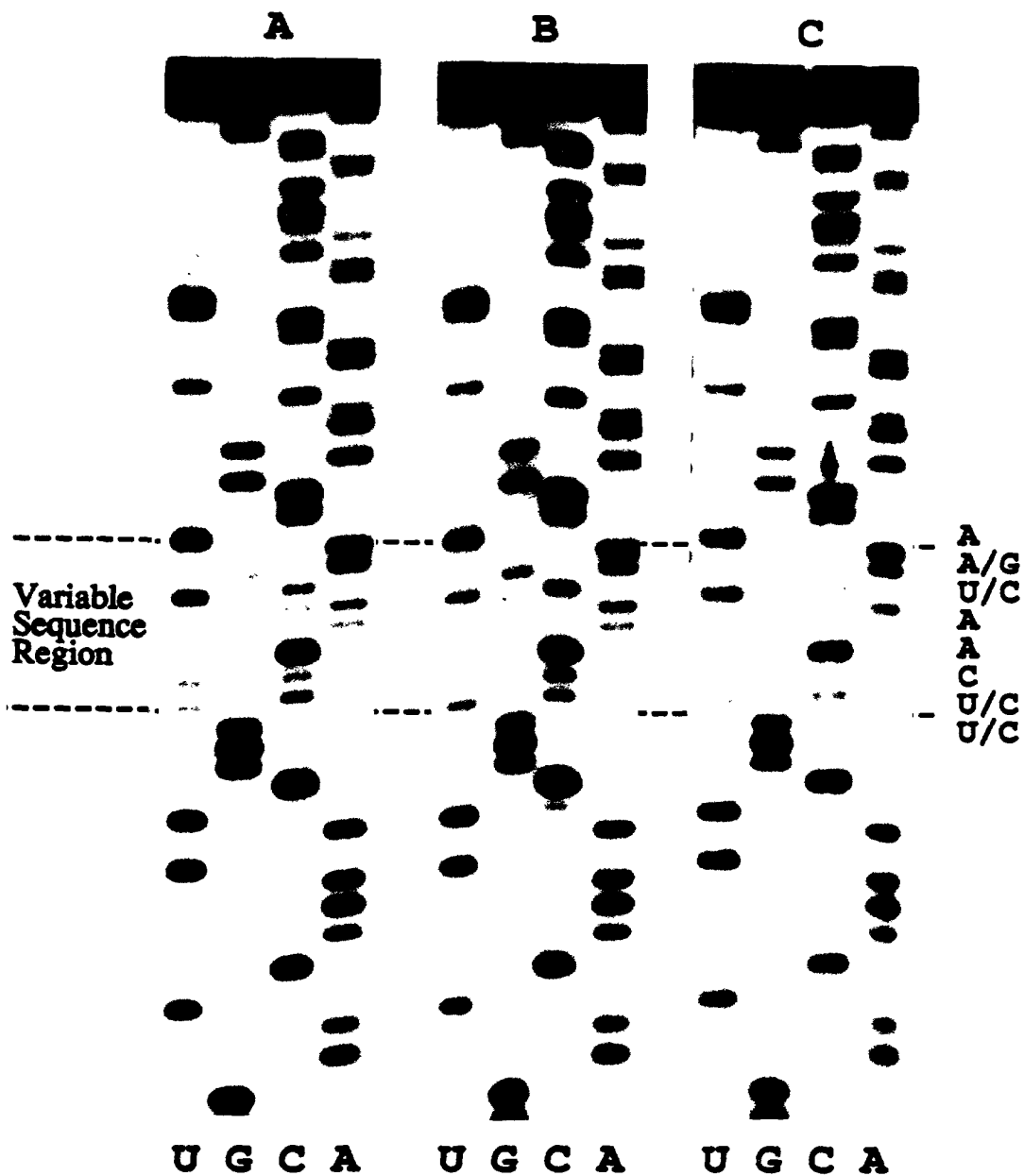


FIG. 5

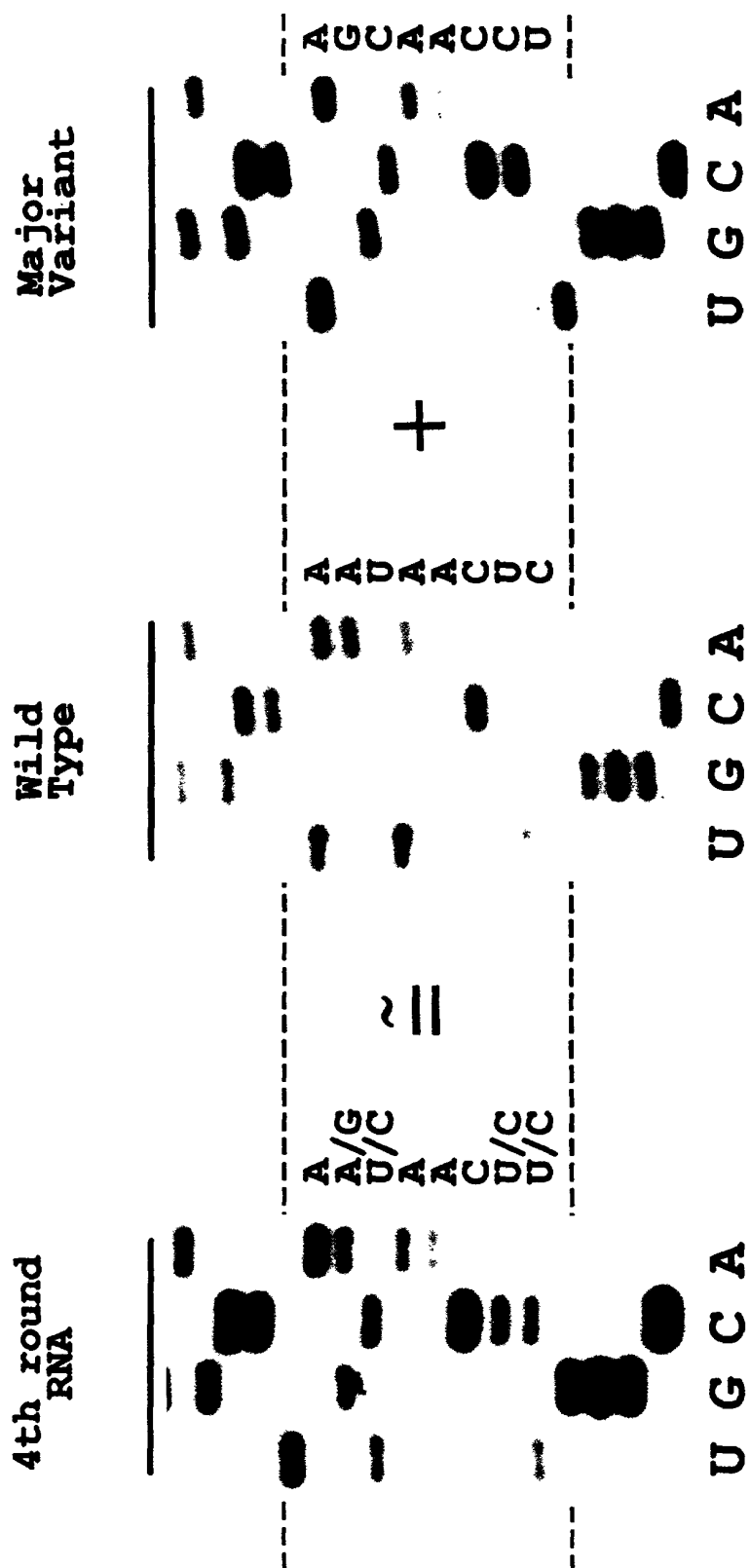
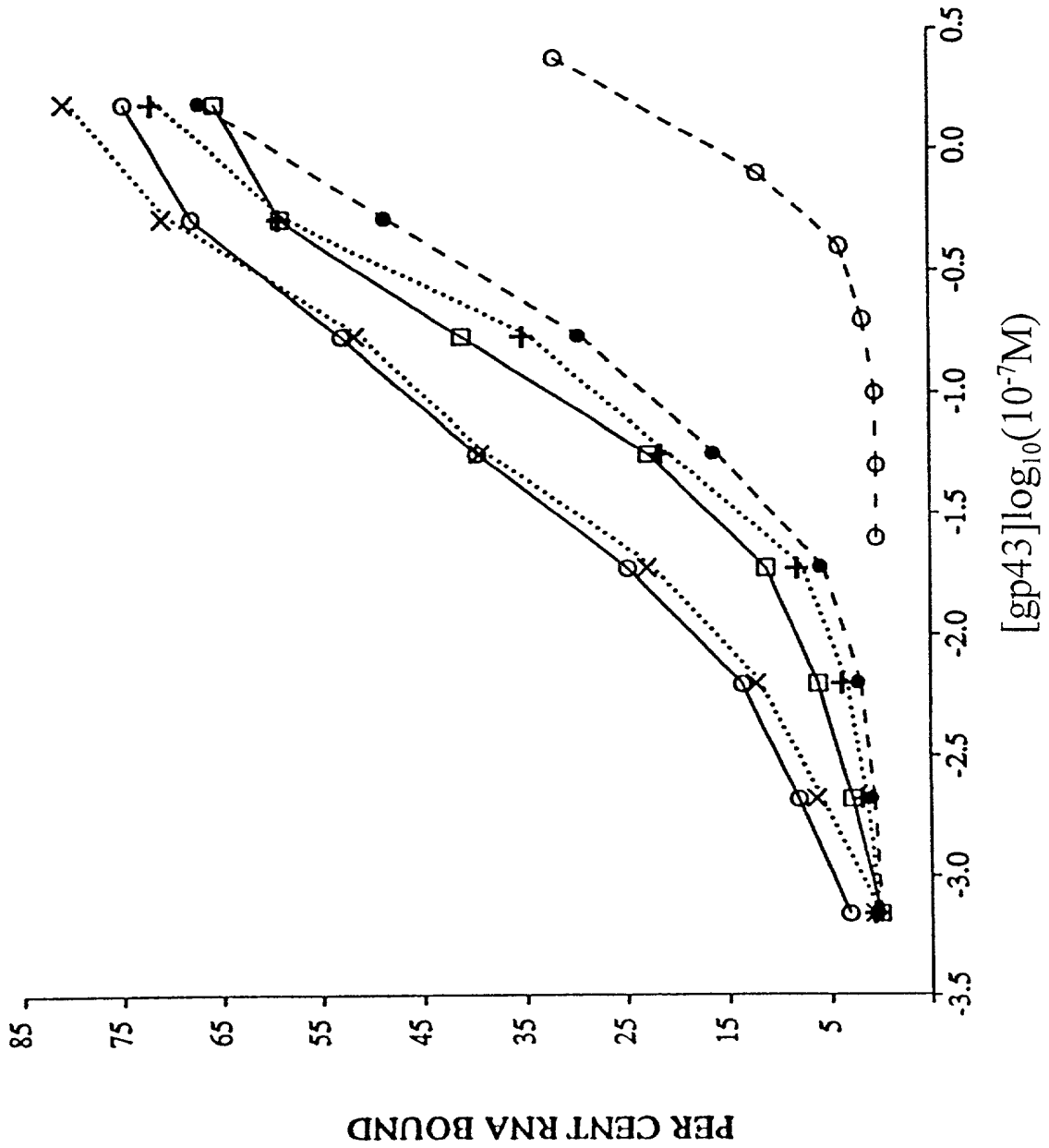
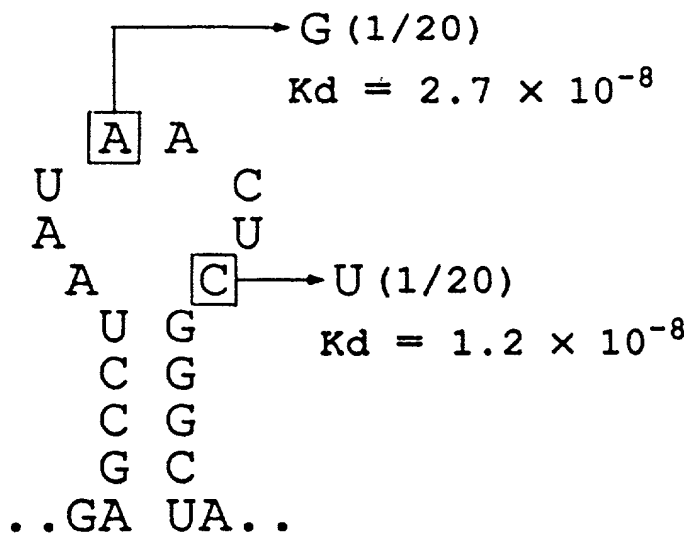
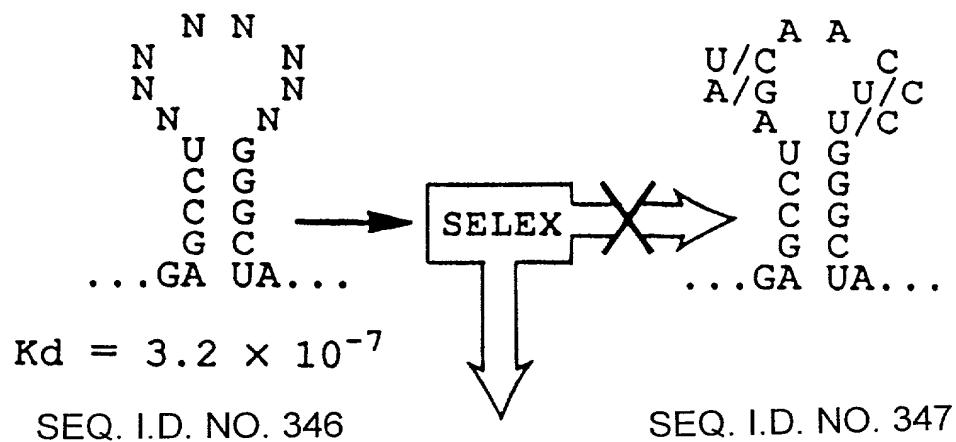


FIG. 6

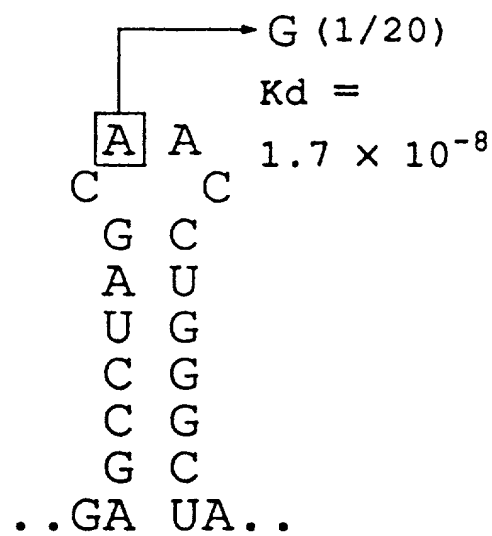




Wild Type

(9/20)

SEQ. I.D. NO. 348



Major Variant

(8/20)

SEQ. I.D. NO. 349

$K_d = 4.8 \times 10^{-9}$

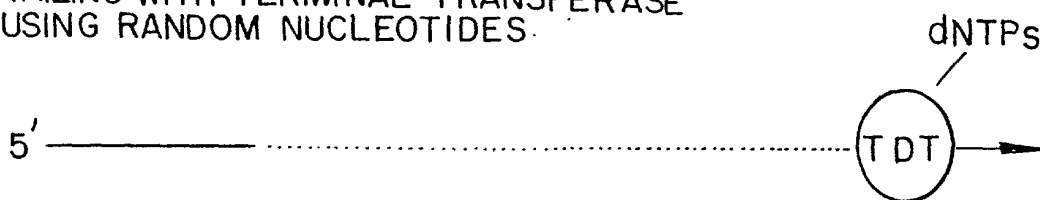
FIG. 7

VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE

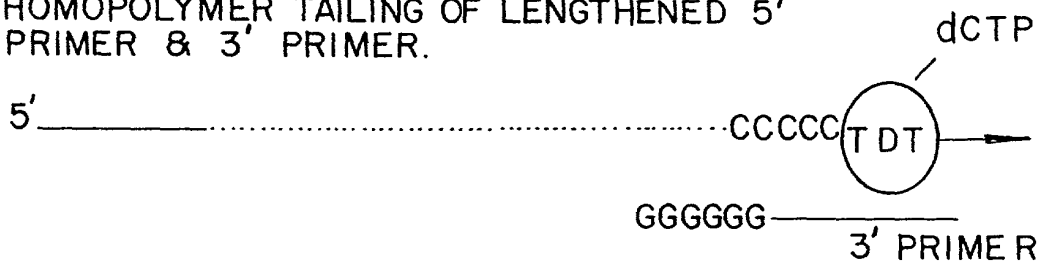
5' PRIMER
 (OR PRIMARY LIGAND SEQUENCE)
 5' ————— 3' 3' ————— 5' 3' PRIMER



TAILING WITH TERMINAL TRANSFERASE
 USING RANDOM NUCLEOTIDES.



HOMOPOLYMER TAILING OF LENGTHENED 5'
 PRIMER & 3' PRIMER.



ANNEALLING & FILLIN

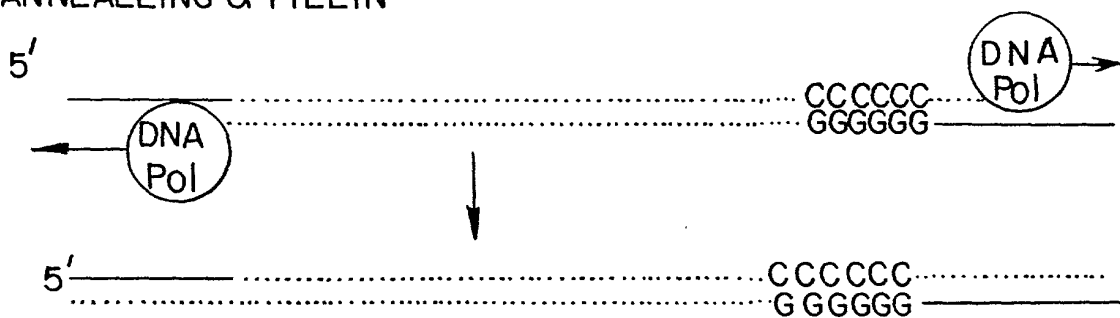


FIG. 8

10037986-101201

"WALKING" BY EXTENDING THE PRIMARY LIGAND.

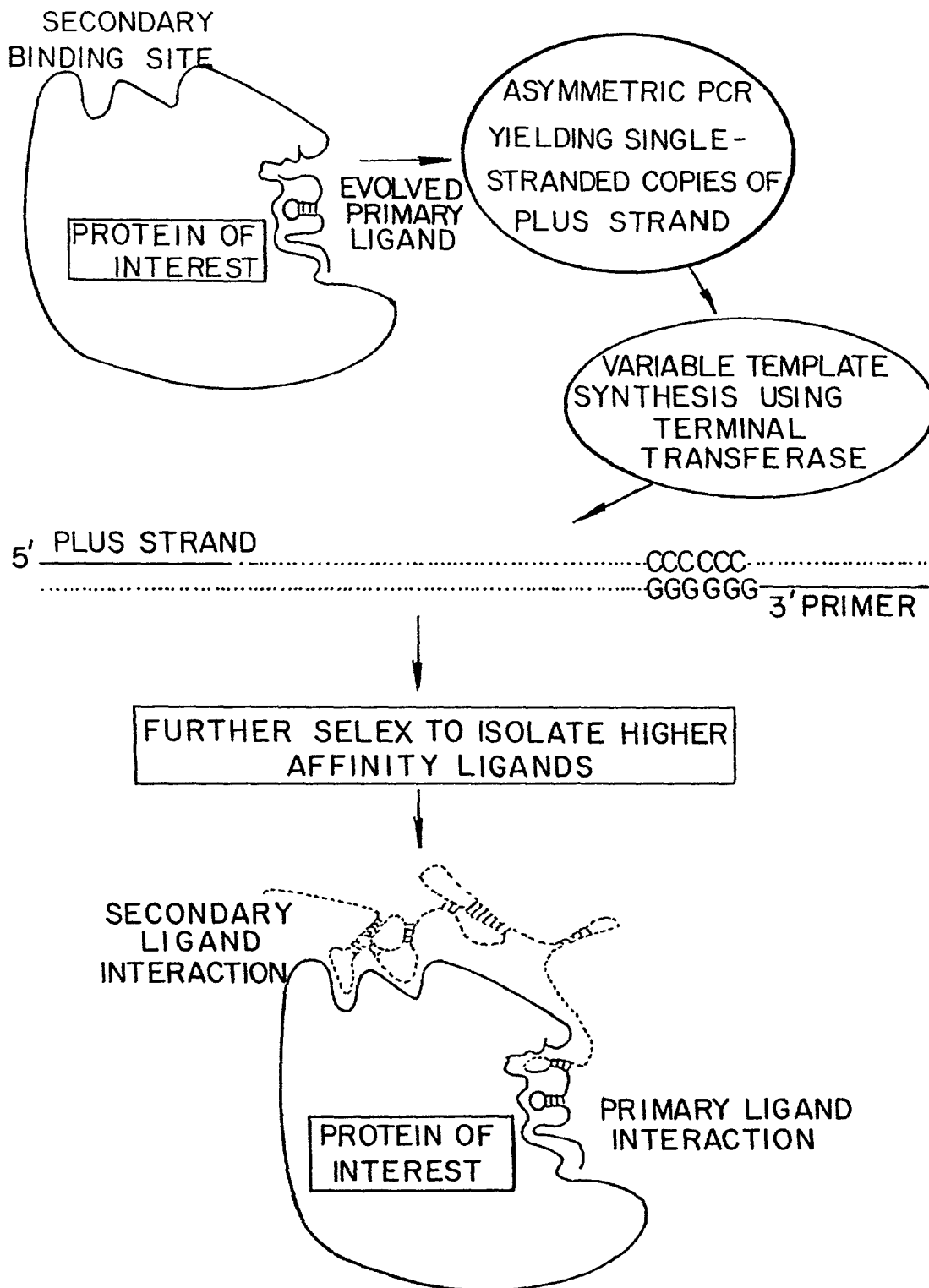


FIG.9

ANCHORING OF BRIDGING OLIGONUCLEOTIDE &
SECONDARY LIGAND EVOLUTION.

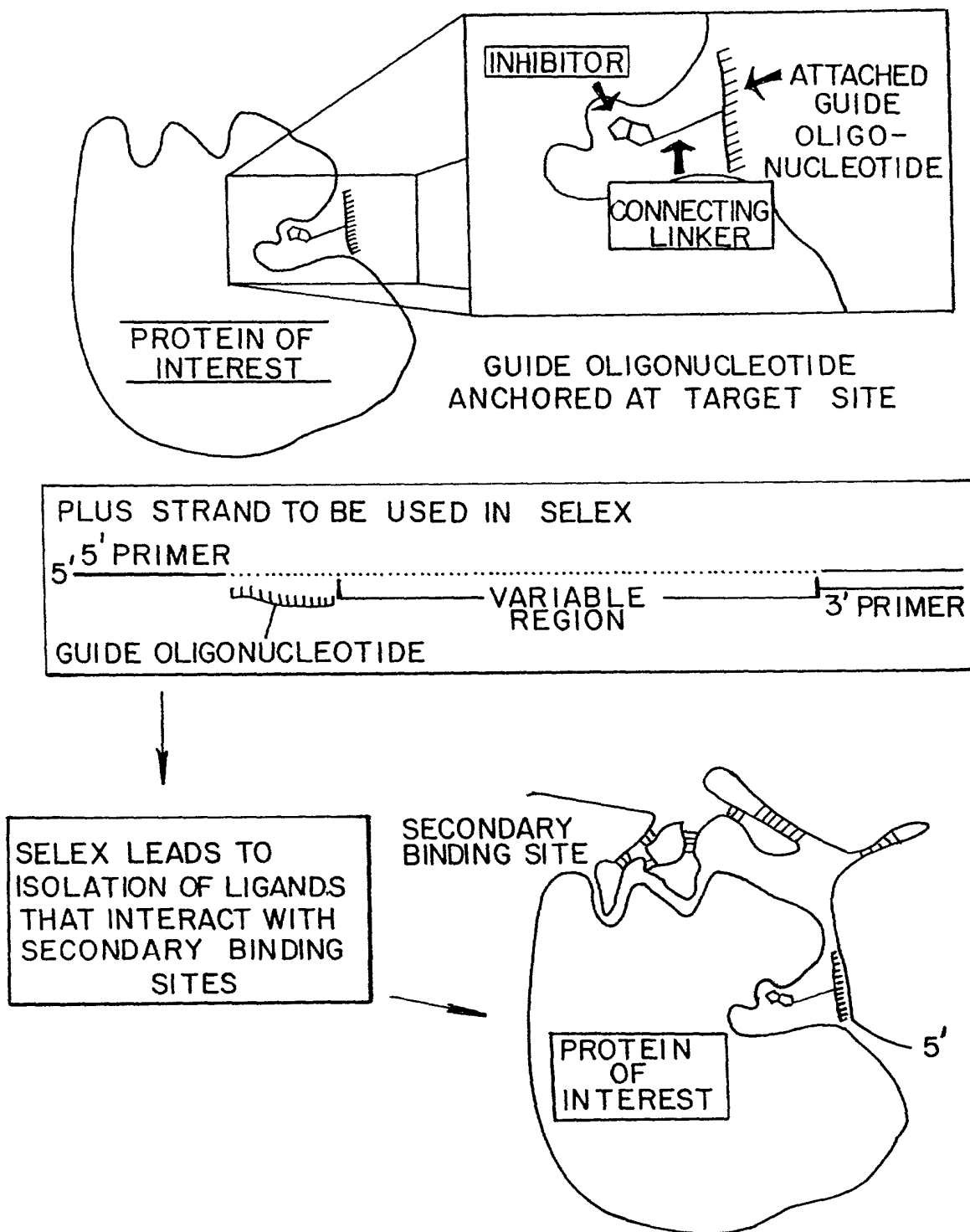


FIG.10

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION.

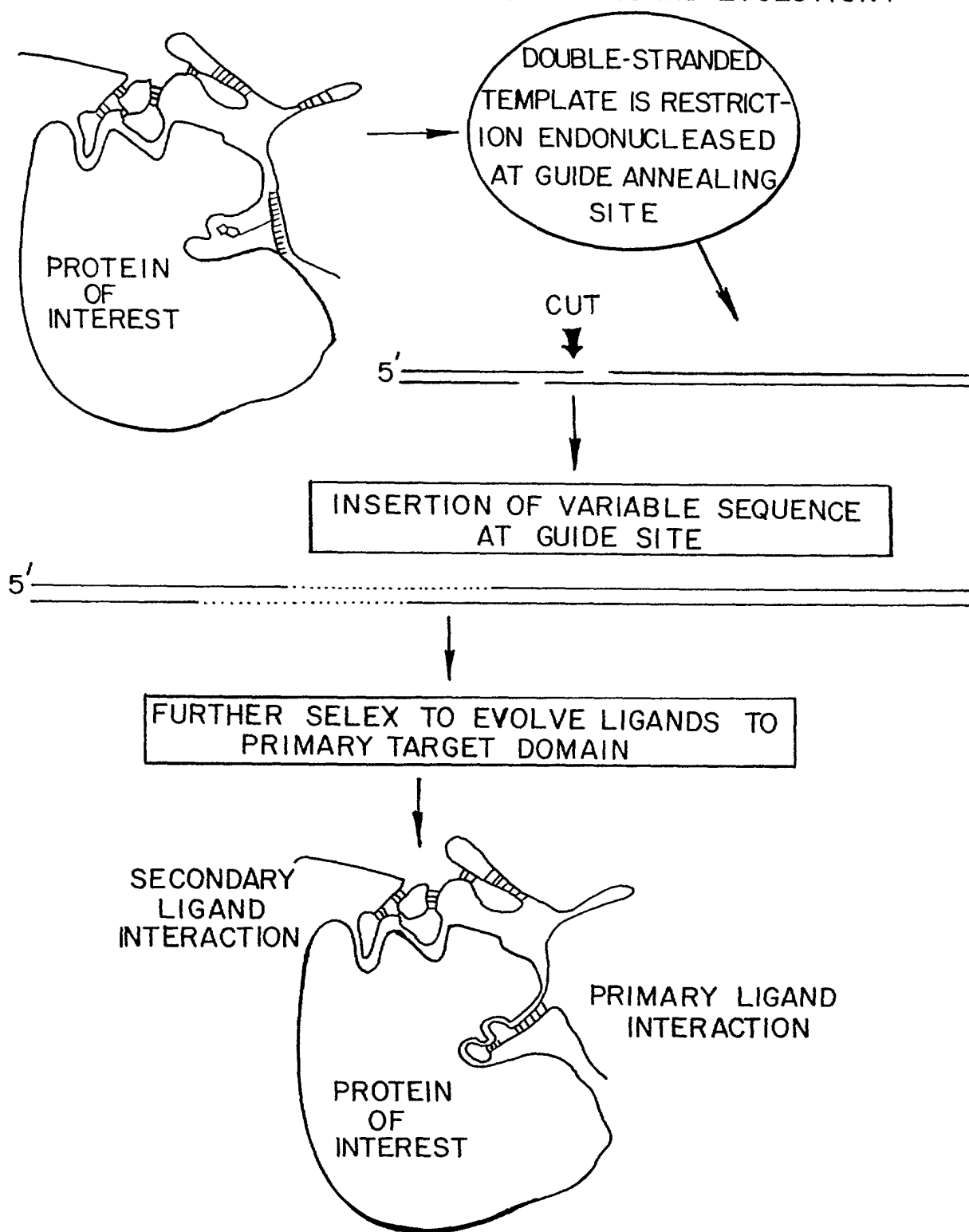
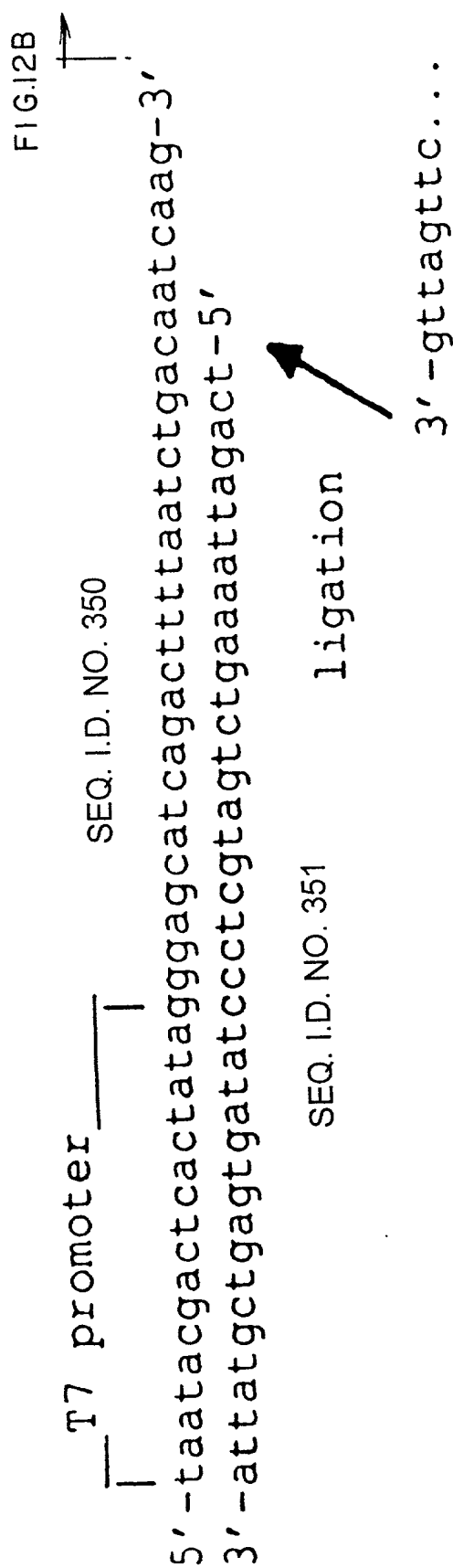


FIG.11



in vitro transcript

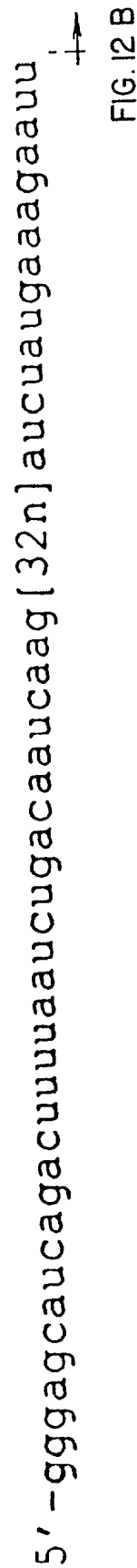


FIG.12A

TTTTT" 986/600T

← 12A

5'-atctatgaaagaattttatatctc-3'

3'-cttaaaatagagataaactttgcctaggcc-5'



ligation

SEQ. I.D. NO. 352

32n...tagatacttt-5'

SEQ. I.D. NO. 353

uuauaucucuauugaaacggauccgg-3'

← 12A

SEQ. I.D. NO. 354

FIG. 12B

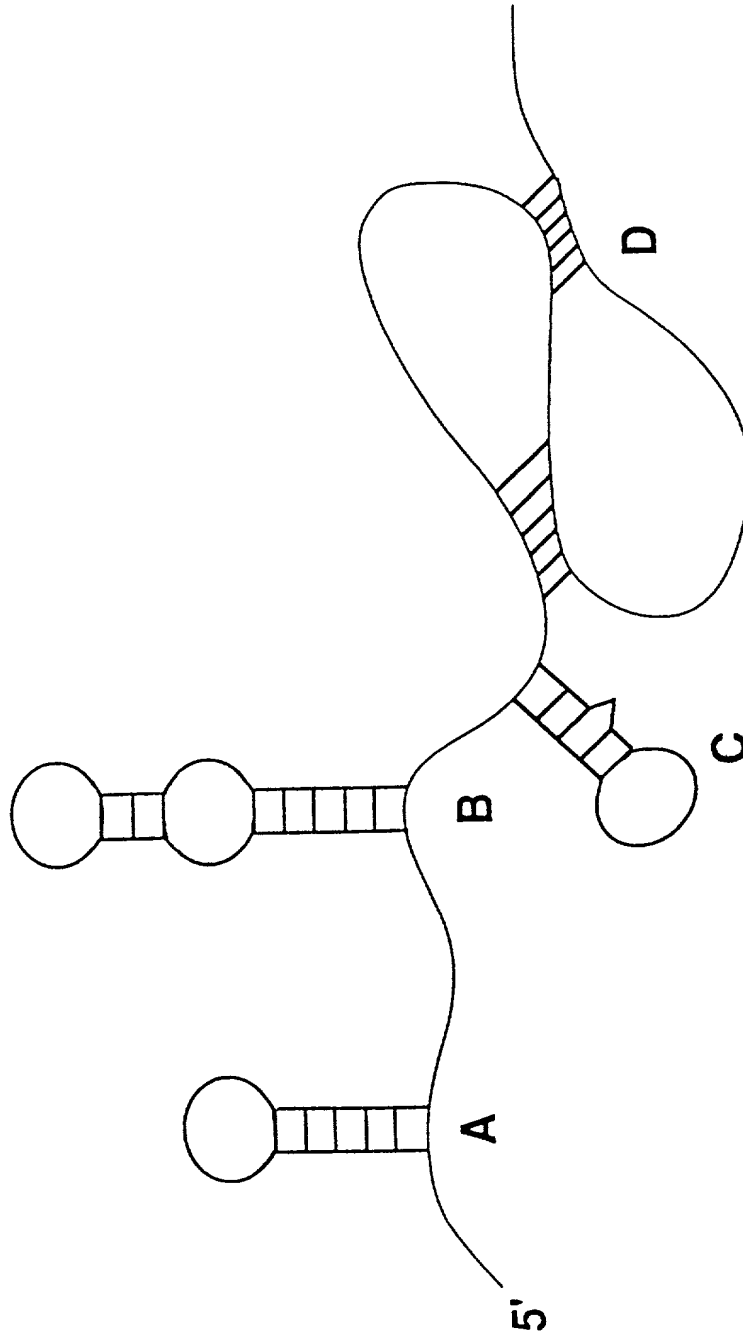
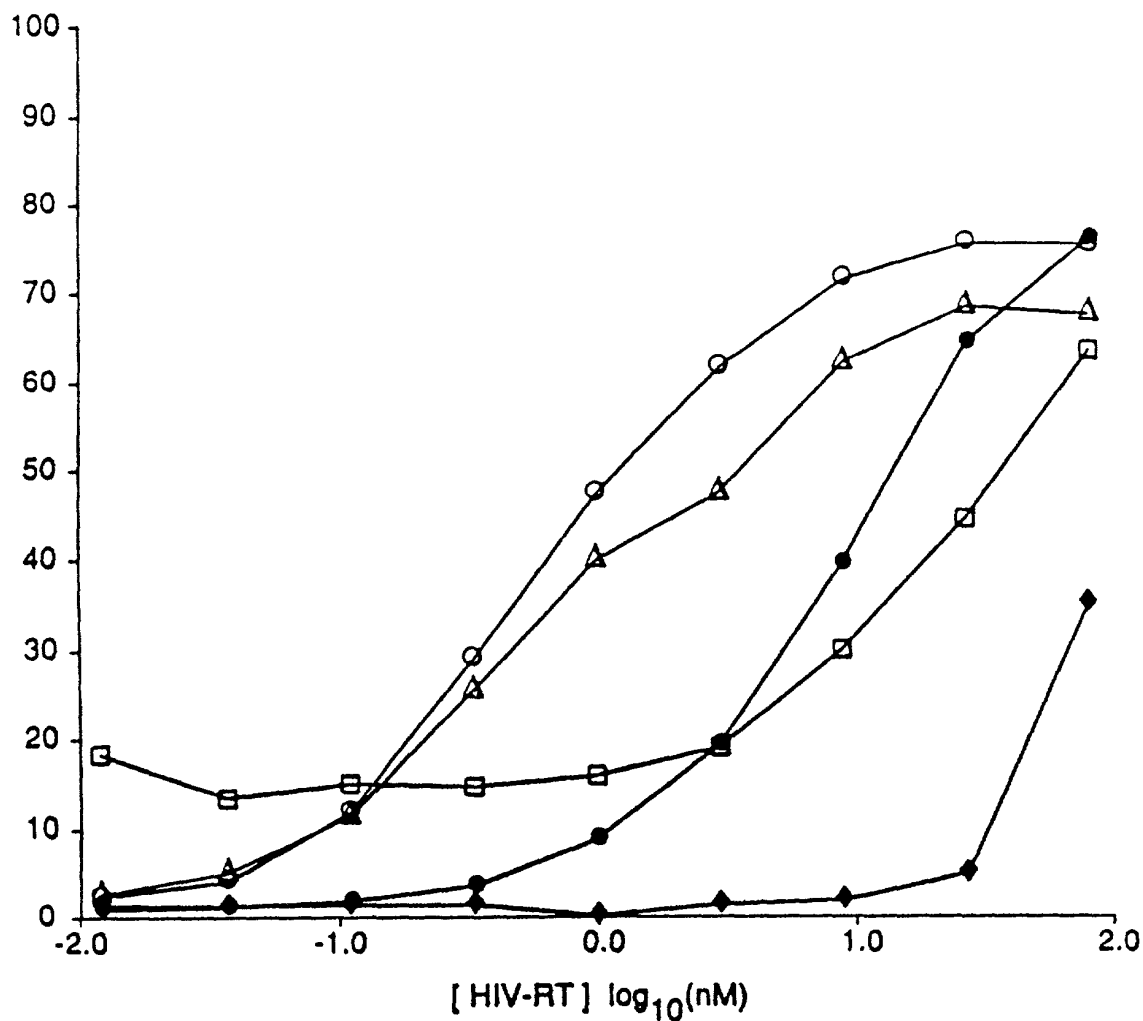


FIG. 13

FIG. 14



Δ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACAaucu (13)

○ 1.3 ucaagAAUAUCUUCCGAAGCCGAACGGGAAAACCGGCAaucu (1)

● 1.3 -----G-----A----- (1)

□ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

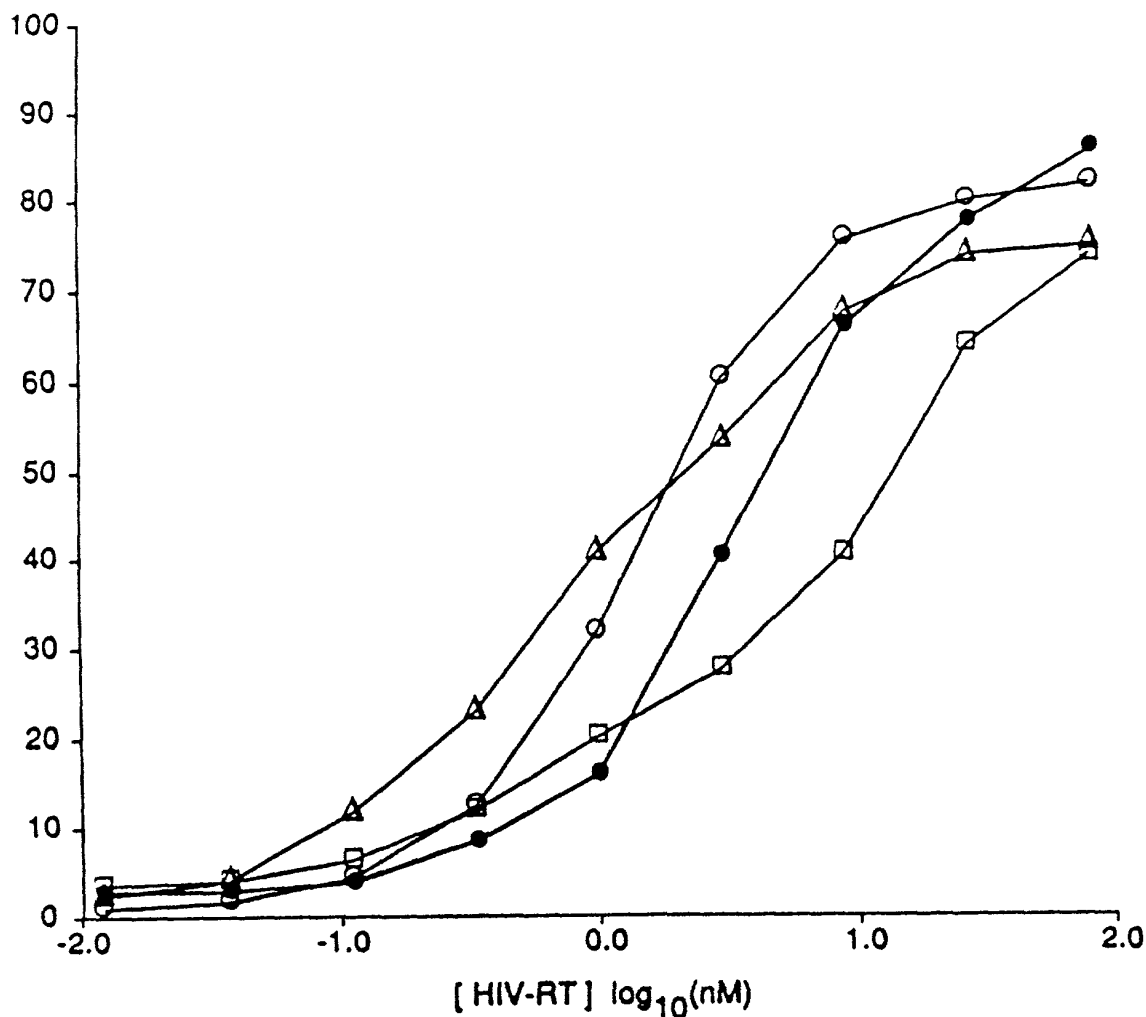
Δ 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

○ 1.3 = SEQ. I.D. NO. 356

□ 1.4 = SEQ. I.D. NO. 358

FIG. 15



ISOLATE

○ 2.1a ucaag--AAUAUA-UCCGAACUCGACGGGAUAACGAGAA-Gaucu (3)

□ 2.2b ucaagUACCCUAGGUGAUAAAGGGAGAACACGUGUGa-cu (13)

● 2.5b ucaagACAGUAUCCGUUCUUGAUCAUCGGGACAAAUGducu (3)

△ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAACUGAACAAUcu (13)

○ 2.1a = SEQ. I.D. NO. 359

● 2.5b = SEQ. I.D. NO. 361

□ 2.2b = SEQ. I.D. NO. 360

△ 1.1 = SEQ. I.D. NO. 362

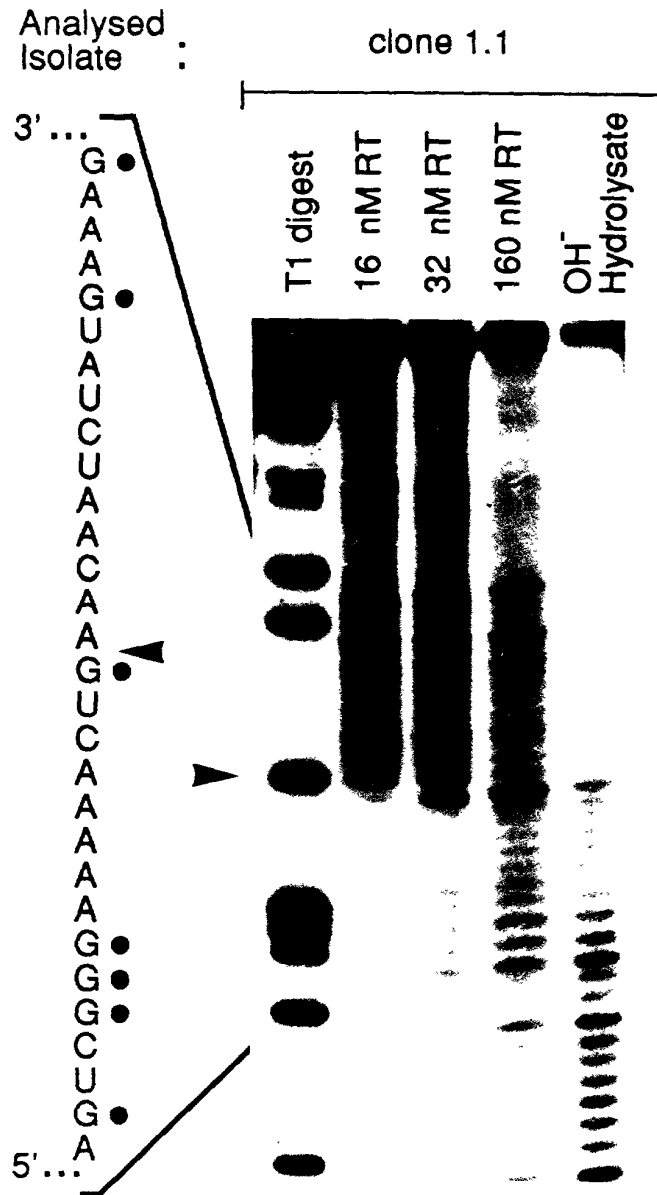


FIG. 16 A

SEQ. I.D. NO. 363

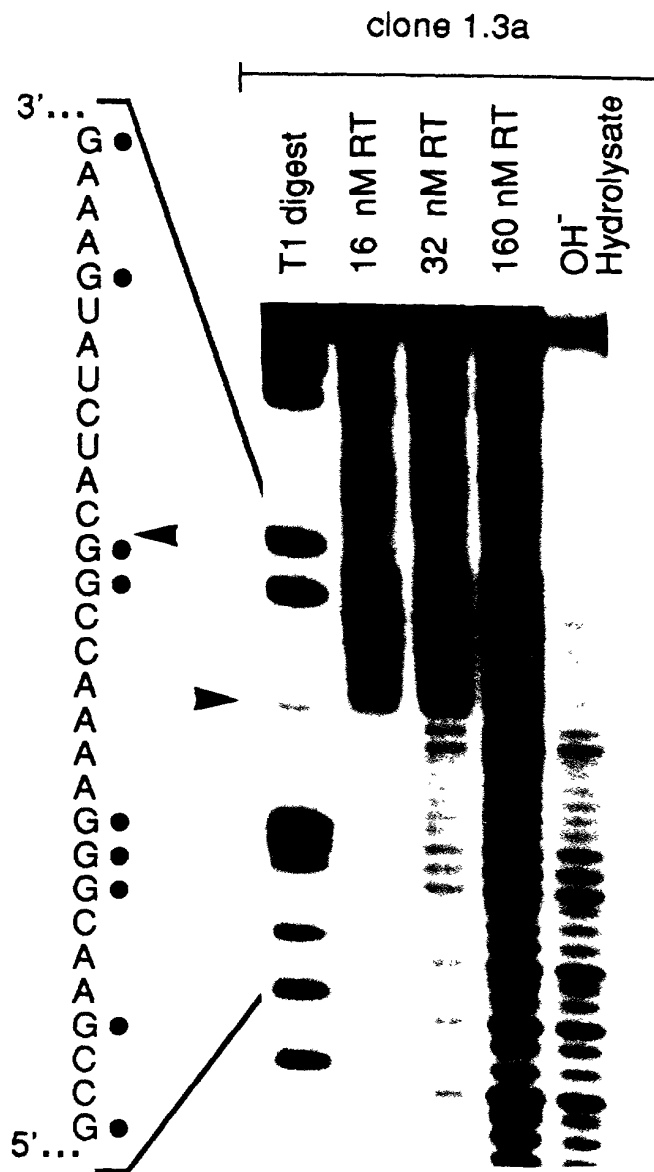
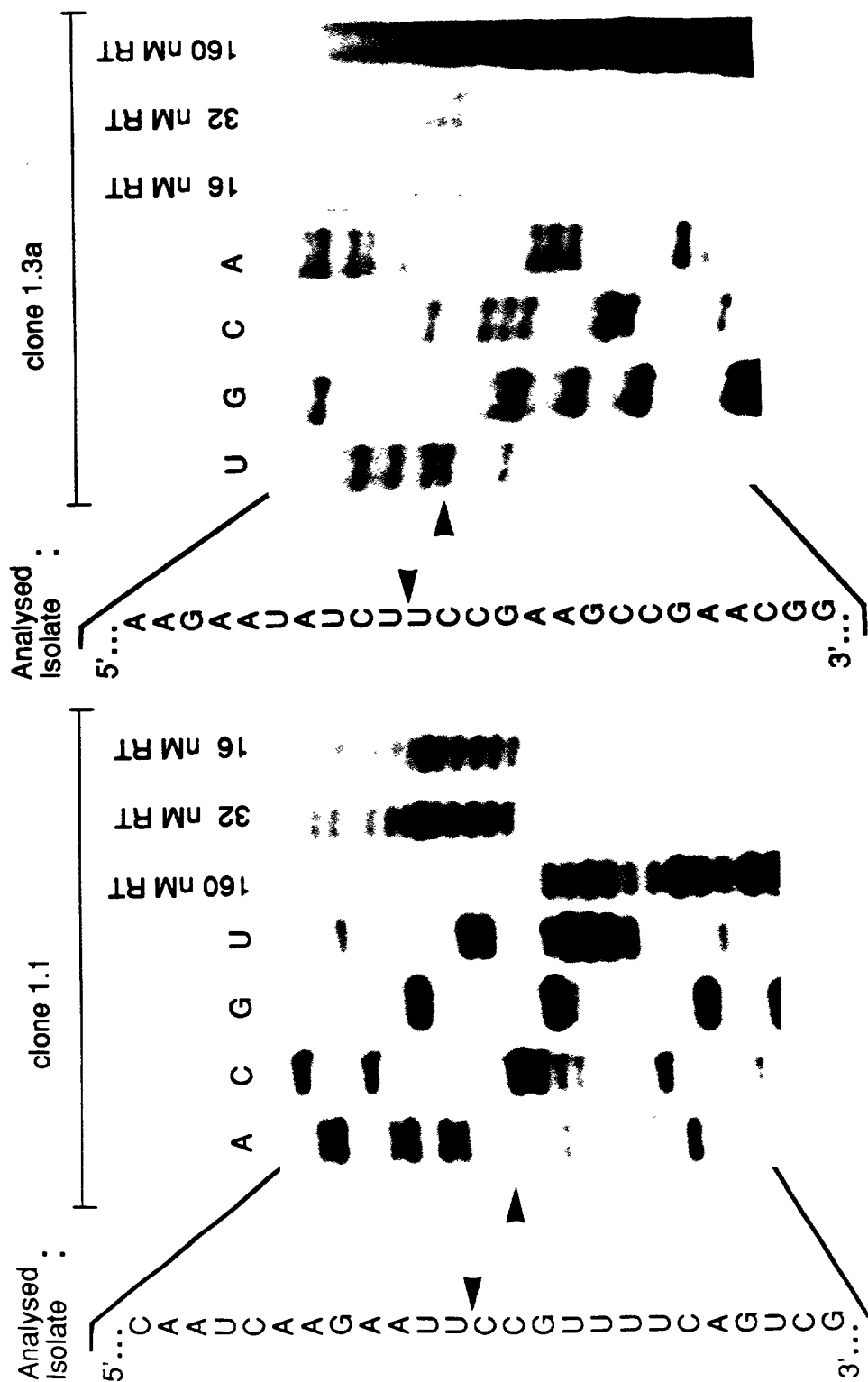


FIG.16 B

SEQ. I.D. NO. 364

FIG. 16 C



SEQ. I.D. NO. 366

SEQ. I.D. NO. 365

FIG. 17B

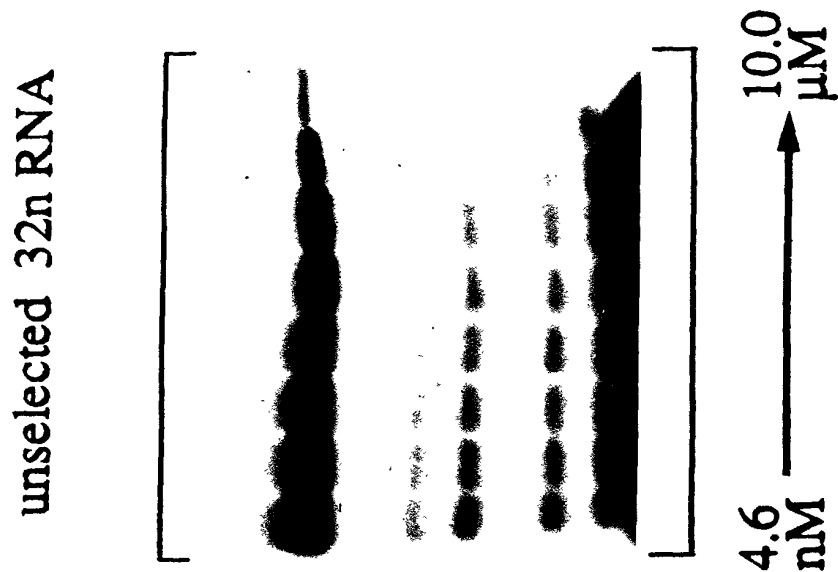


FIG. 17A

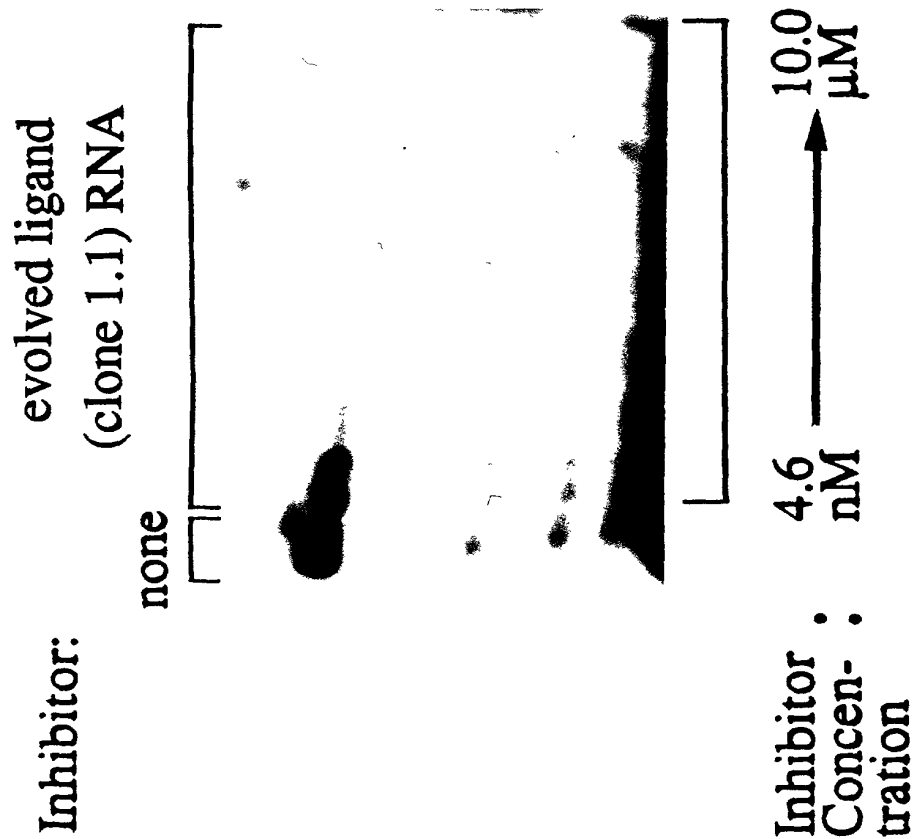


FIG. 18

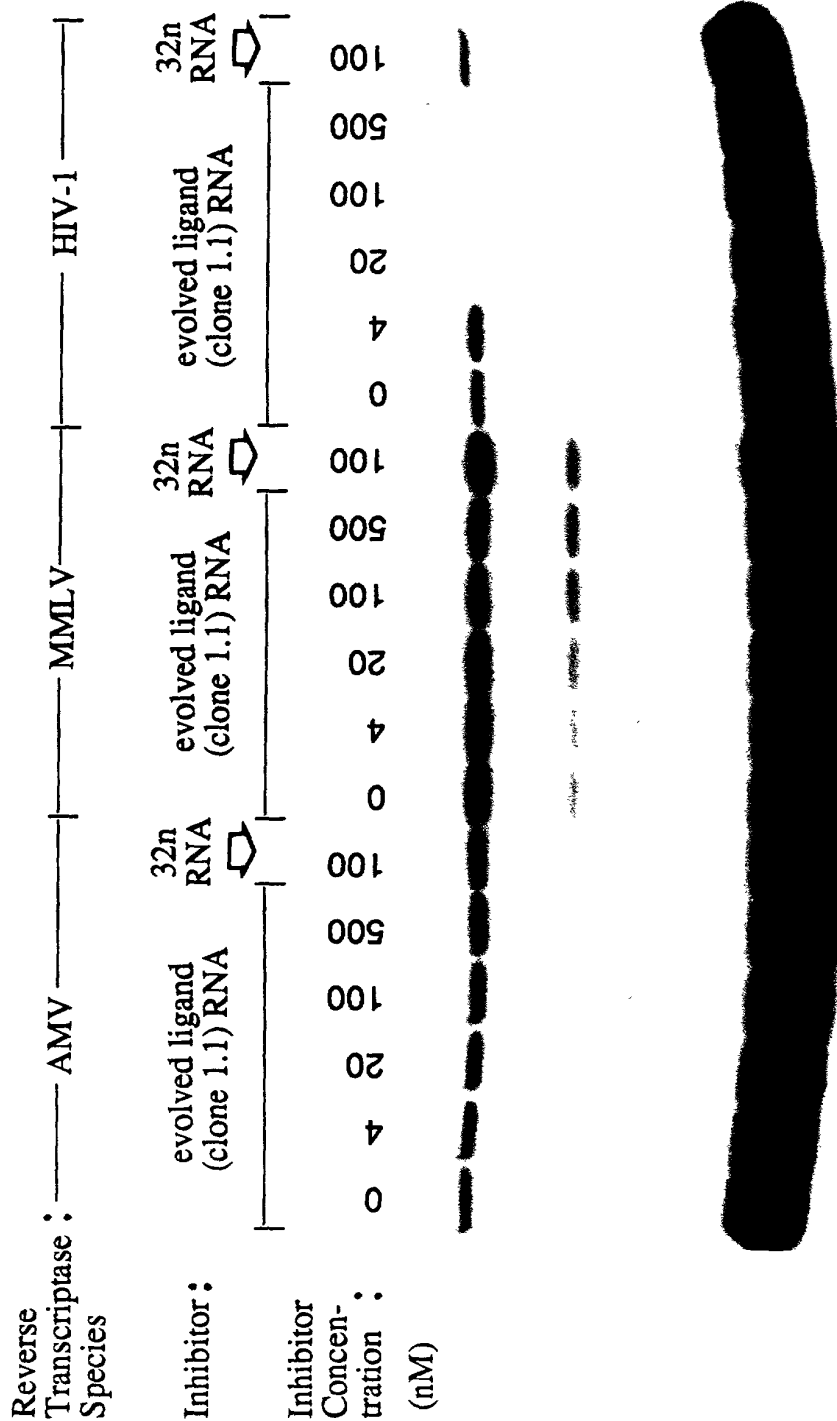
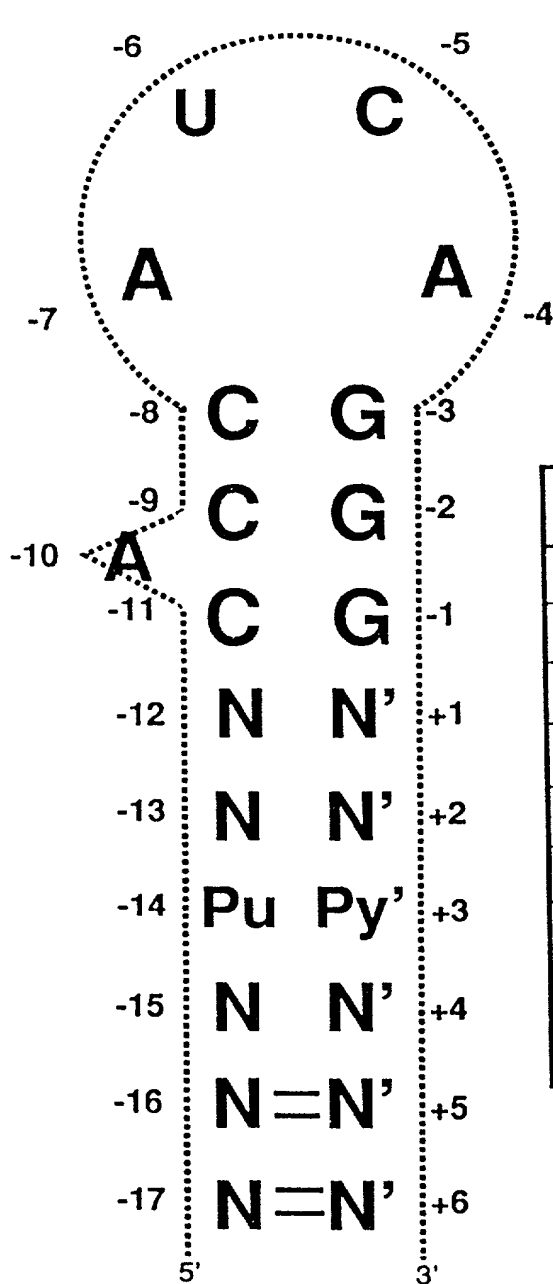


FIG.19B



	A	C	G	U
-4	36	0	0	0
-5	0	36	0	0
-6	4	3	1	28
-7	36	0	0	0
-10	36	0	0	0

	AU	CG	UA	GC	UG	GU	Bulge	END
-8/-3	0	24	0	12	0	0	0	0
-9/-2	0	25	0	10	1	0	36	0
-11/-1	0	24	2	10	0	0	0	1
-12/+1	8	1	8	10	7	1	3	3
-13/+2	6	5	8	9	3	1	3	4
-14/+3	9	0	4	10	2	3	6	8
-15/+4	4	0	9	6	0	1	0	2
-16/+5	10	1	2	1	1	3	1	1
-17/+6	0	4	6	1	4	2		

FIG.19C

FIG.19A

SEQ. I.D. NO. 367

FIG.20

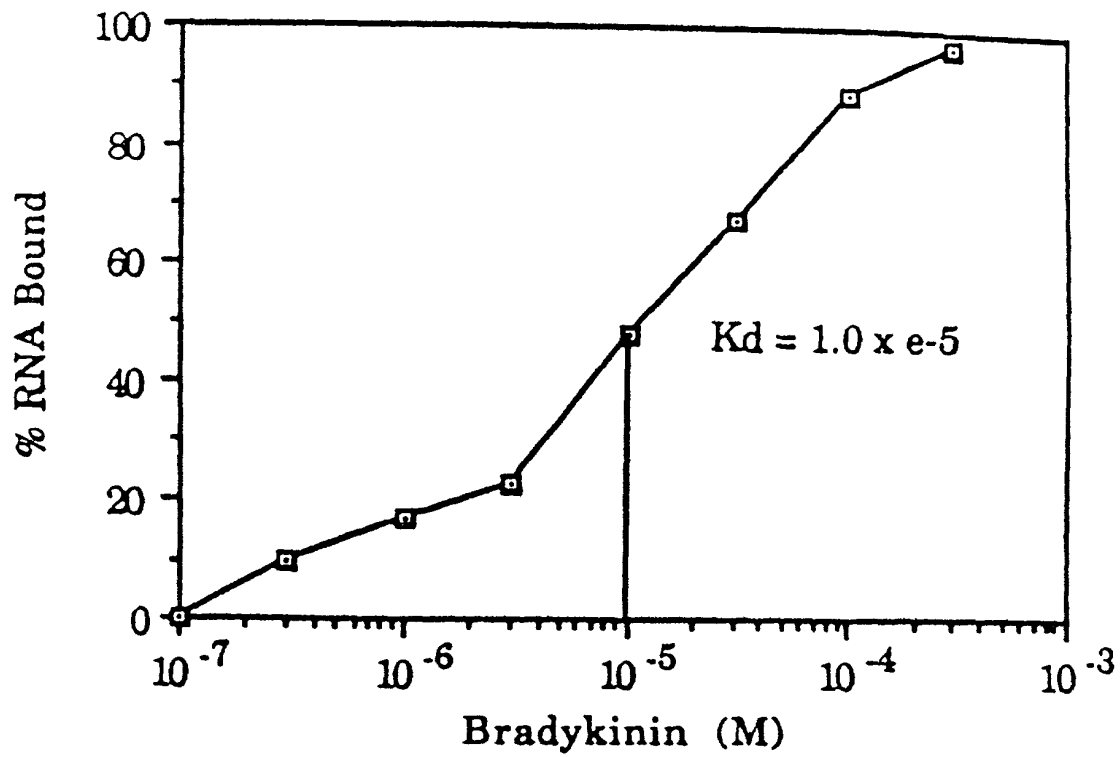


FIG.2IA

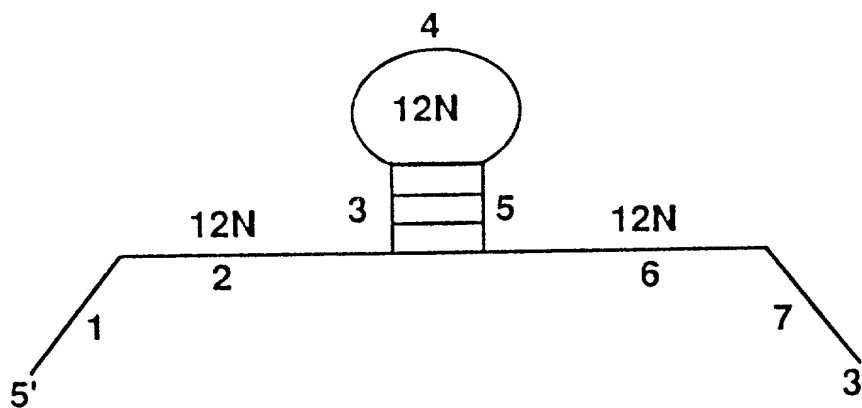
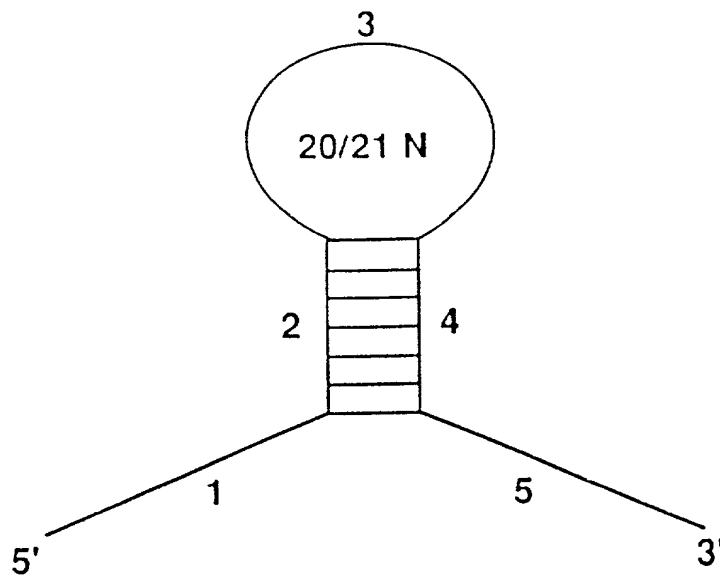


FIG.2IB

FIG. 22

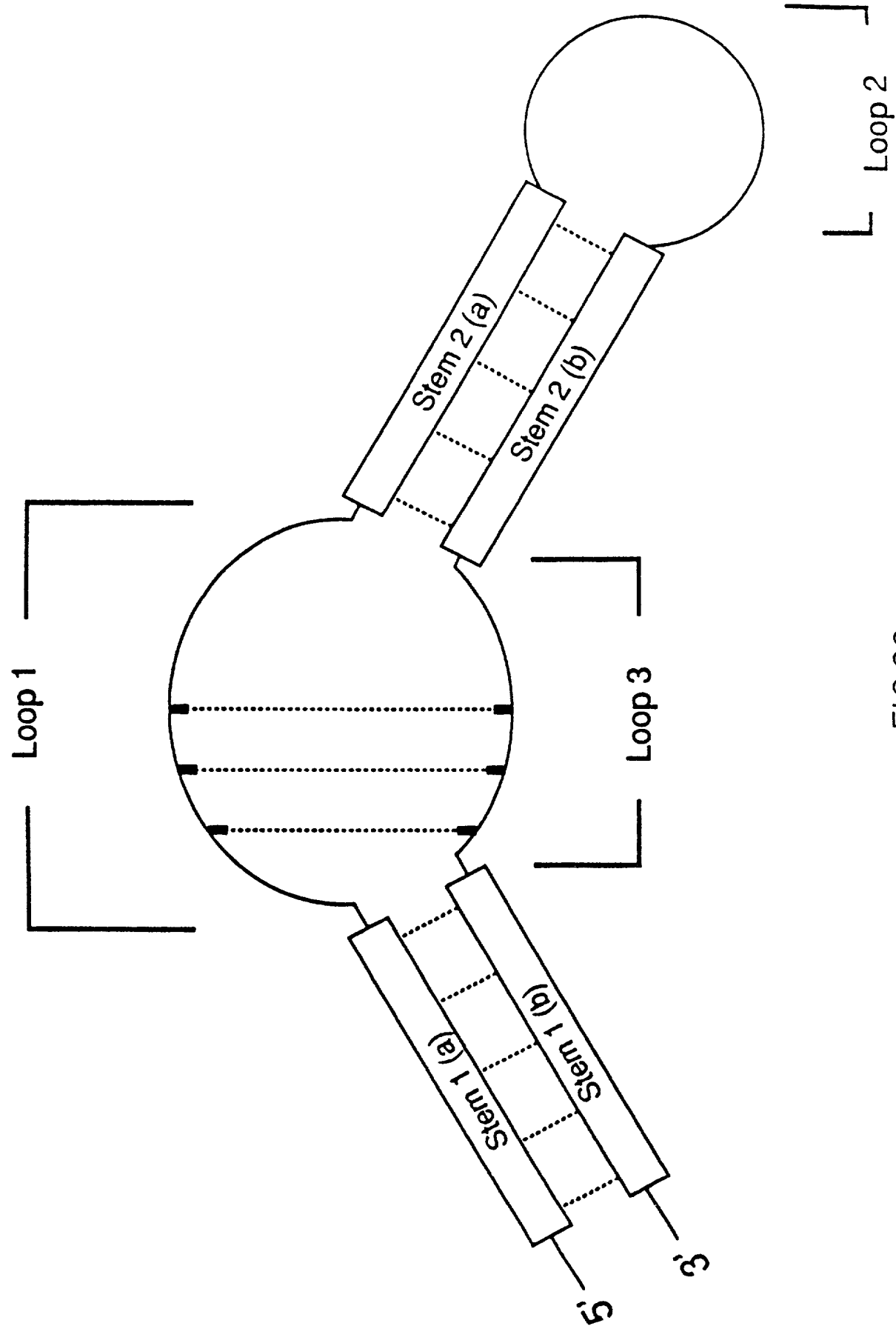


FIG.22

Motif I (6a)

UUGAGAAA G
 5' ...GGUGCA ||| CAC U (NUCLEOTIDES 2-38 OF SEQ. I.D. NO. 301)
 3' ...ucuaUGU ||| GUG U
 --CUCA-G U

Motif III (9a)

CC UUGaucua-
 A GG ||||| uga-3'
 A CC ||||| GCUU-5'
 UU --CUAGUAA

SEQ. I.D. NO. 369

Motif II (1c)

AAGAUU UCU
 5' ...AGAUG CAGC
 3' ...ucuaC GUCC A
 -ACA-G UAG

SEQ. I.D. NO. 368

WT (Motif II-like Domain)

U ACGGUA
 A GACGCUG || CA.....3'
 CUGCGAC || GU.....5'
 A -GCG-G

SEQ. I.D. NO. 370

FIG. 23

FIG. 24

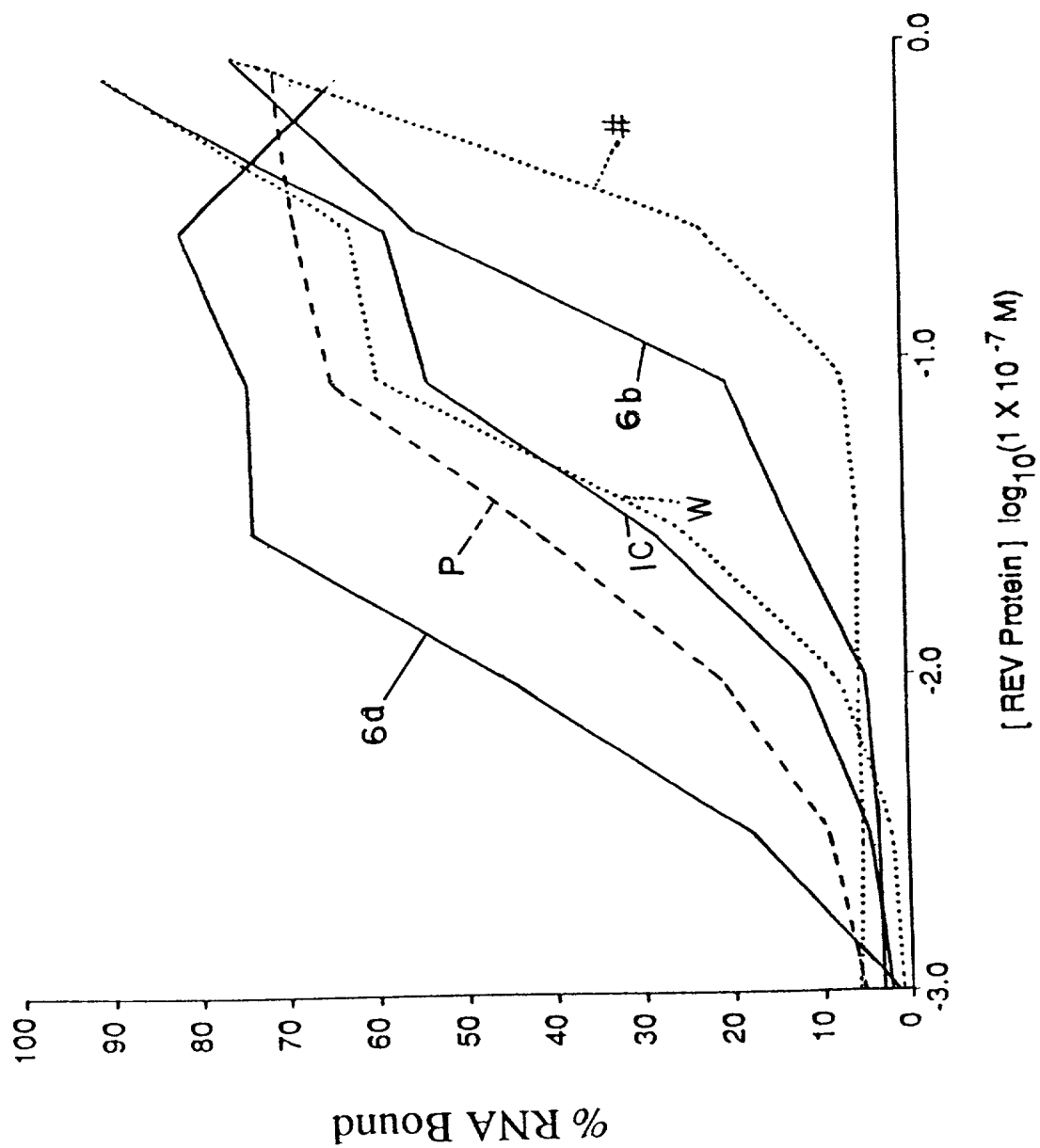


FIG. 25

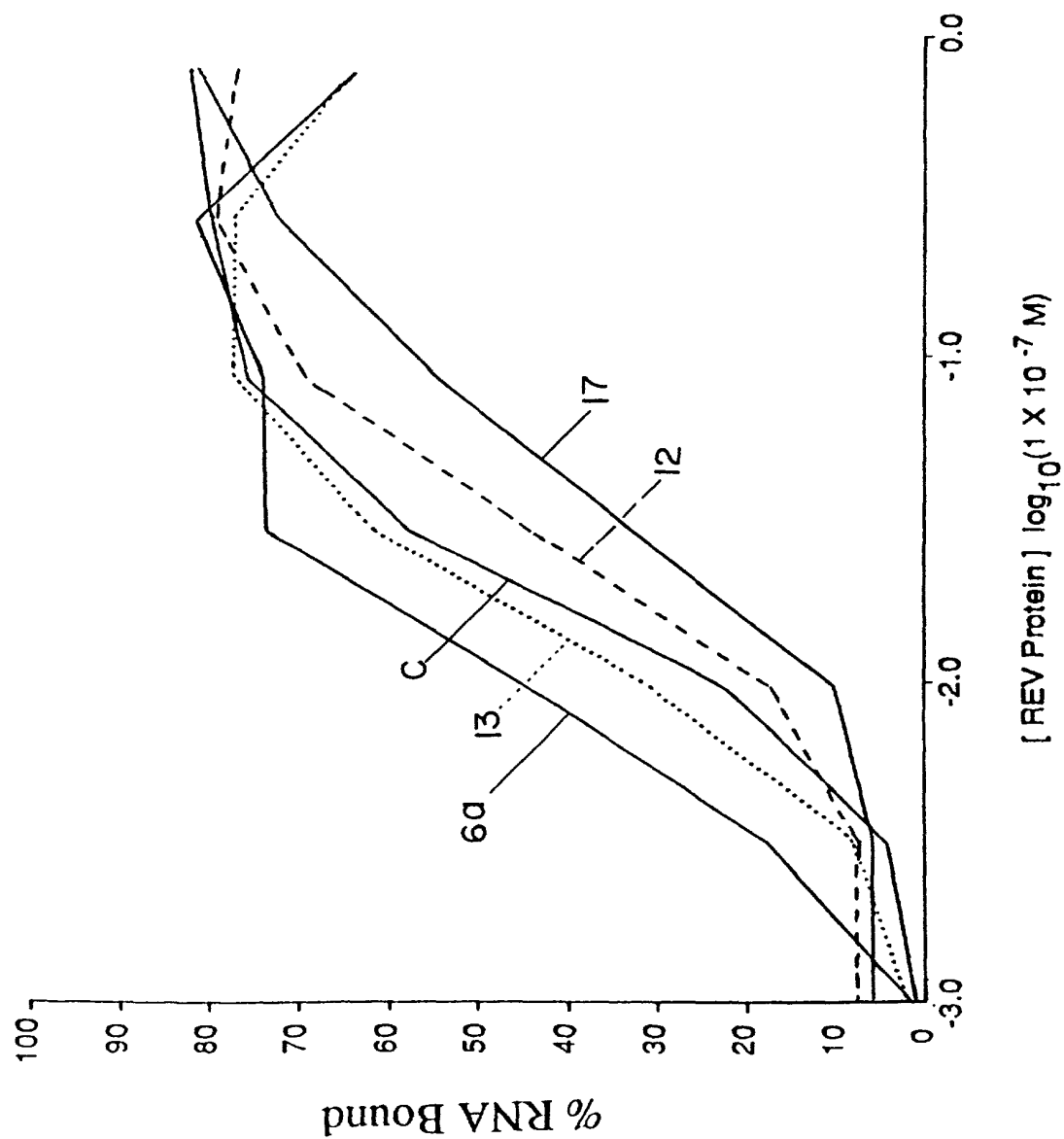
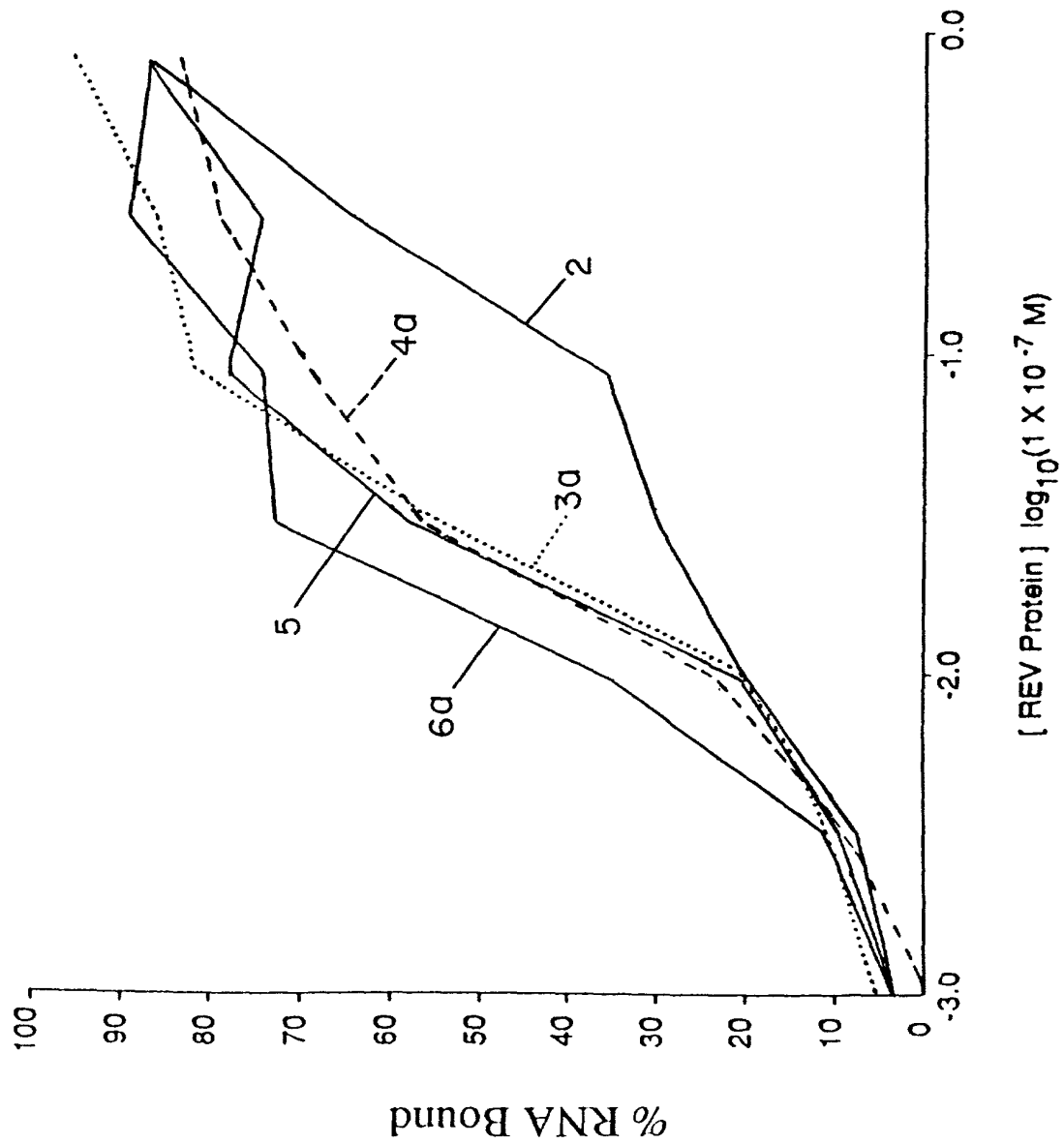


FIG. 26



FOOTNOT 9862E00T

FIG. 27

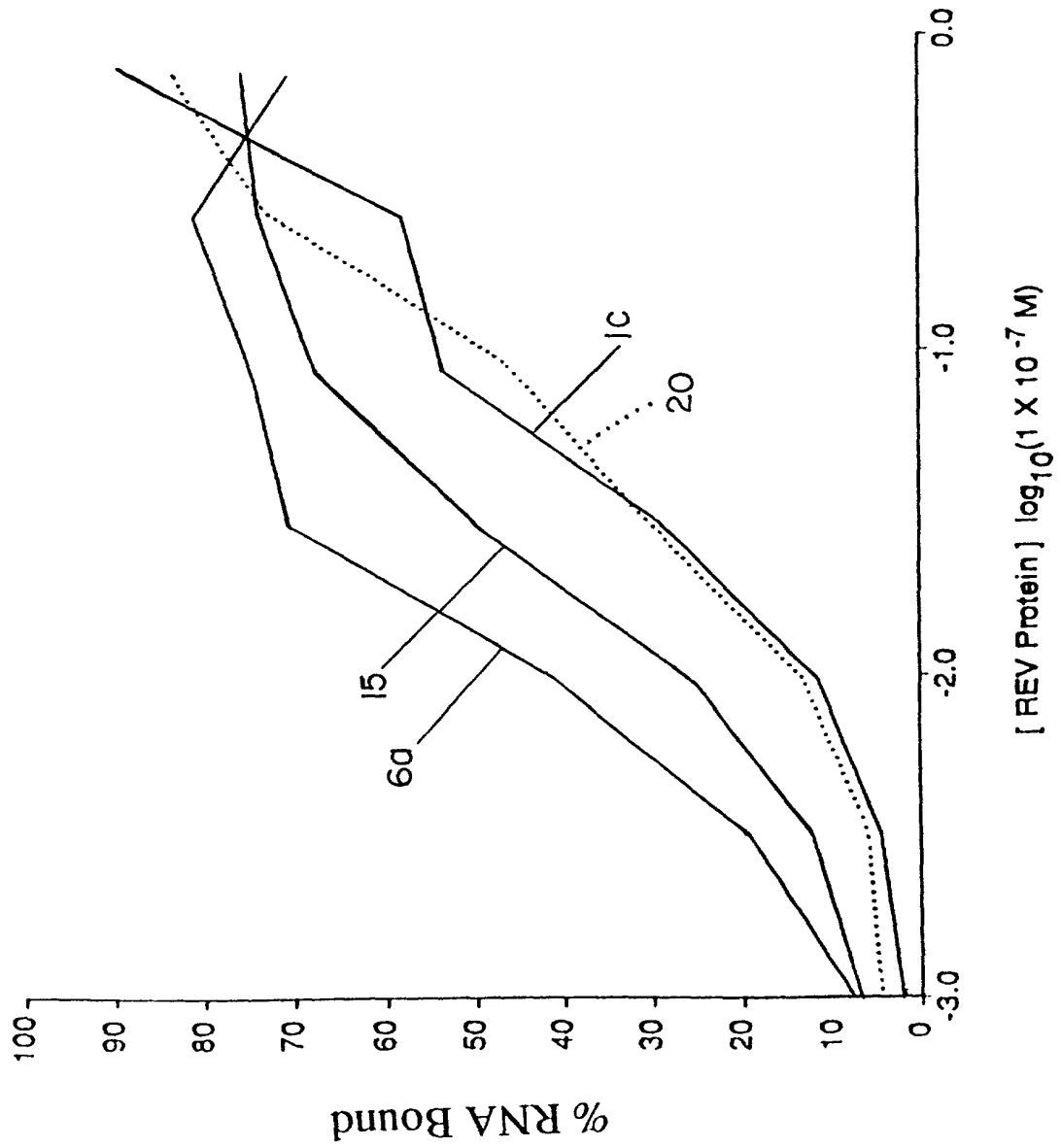
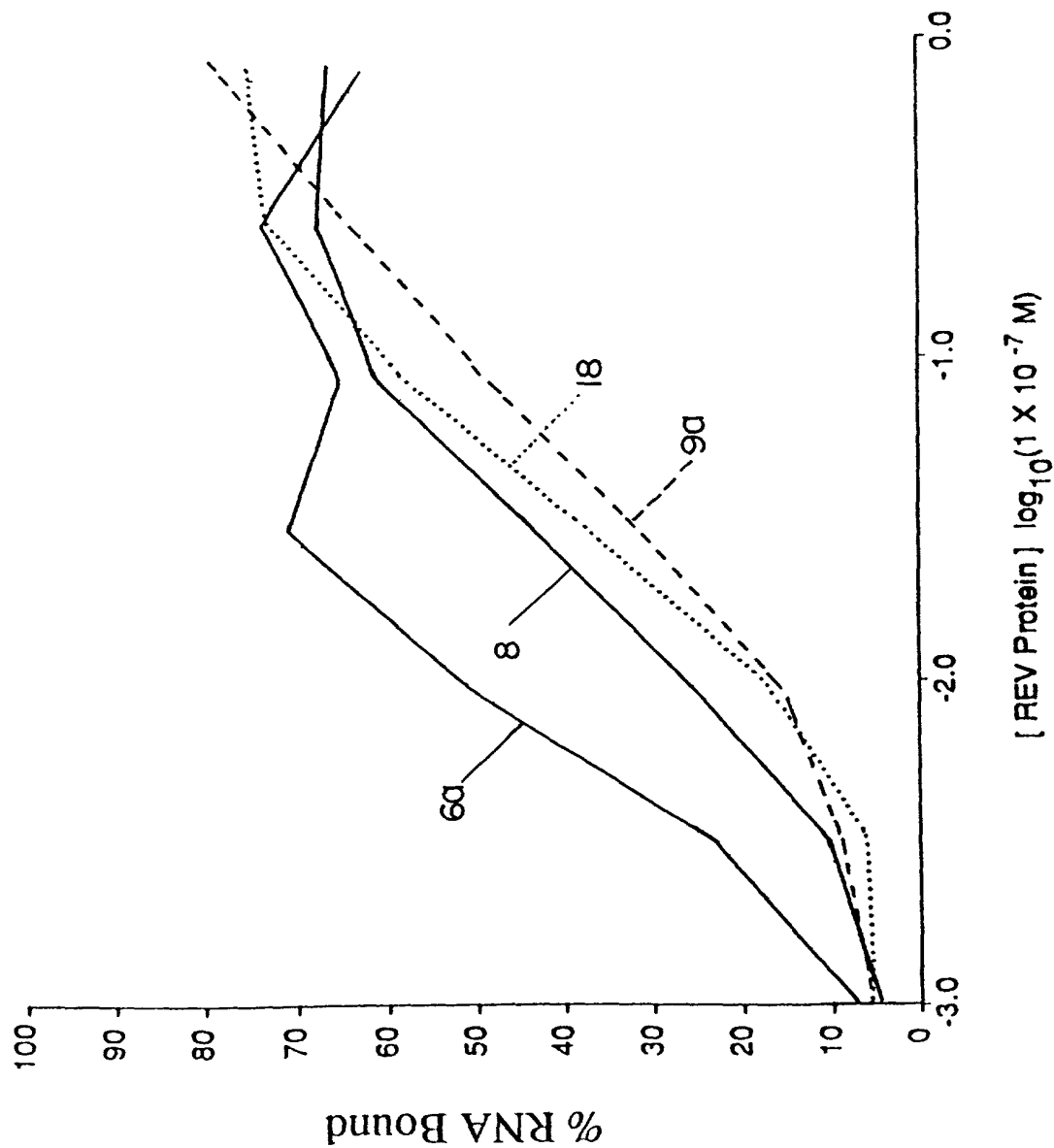


FIG. 28



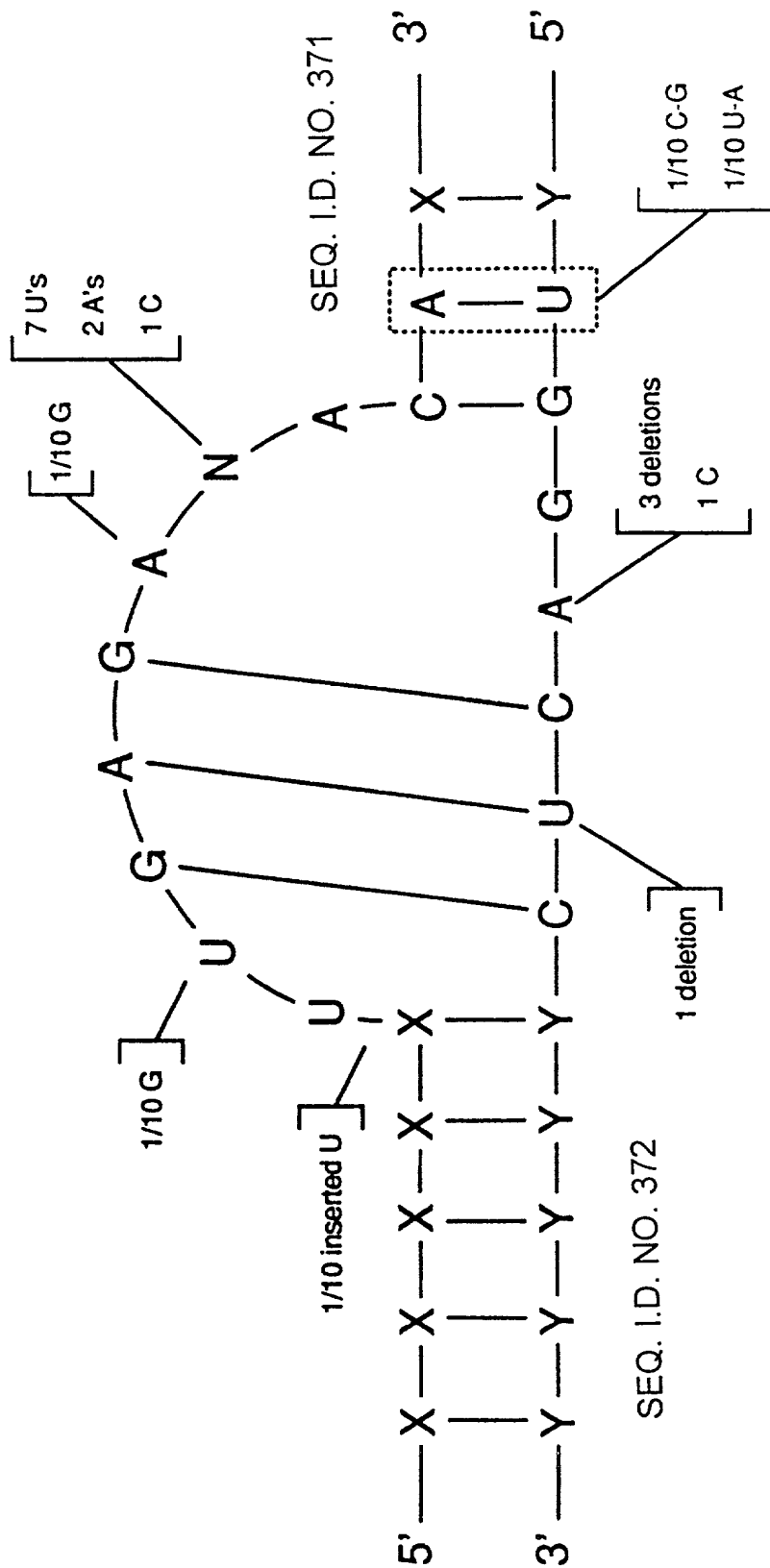
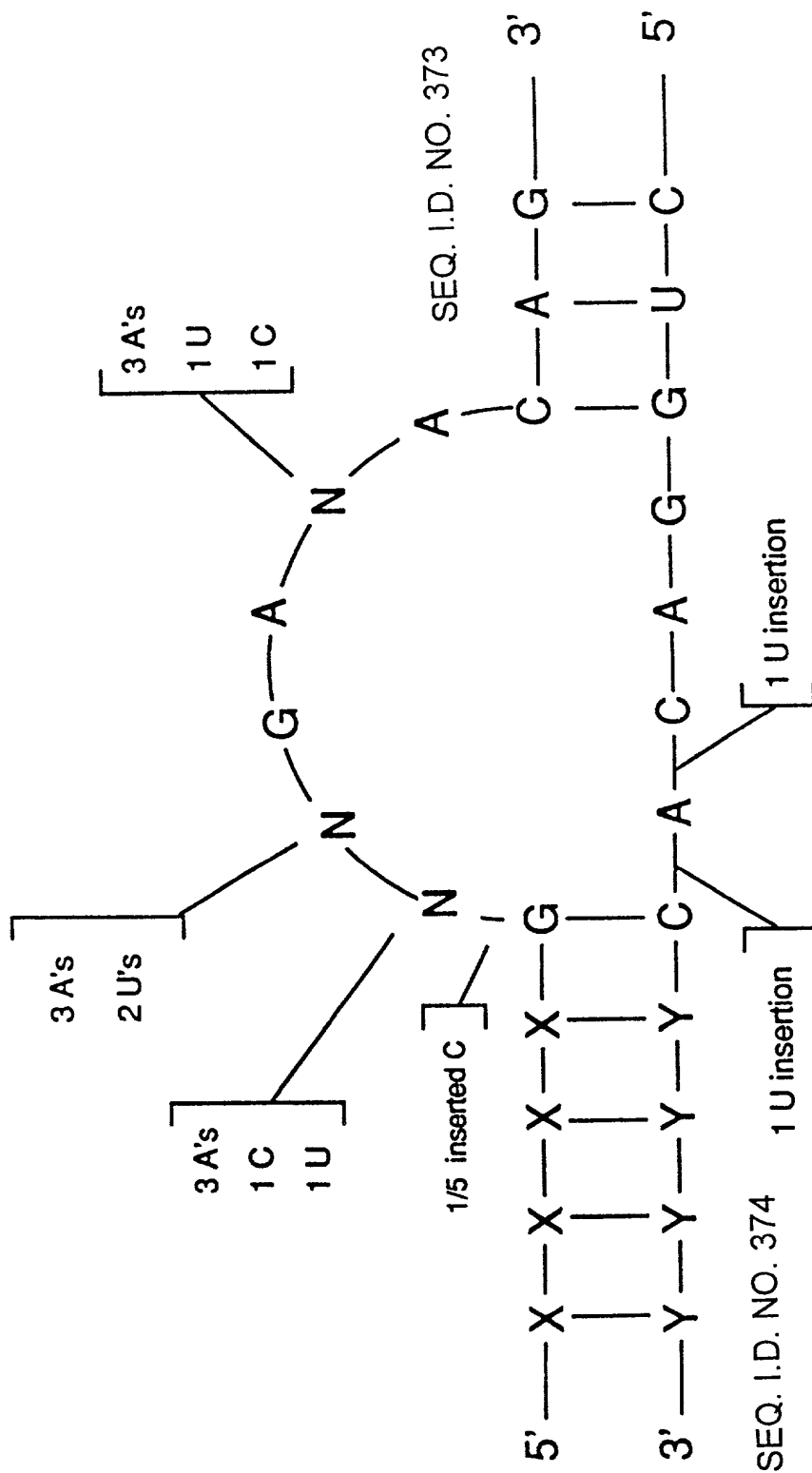


FIG. 29

FIG. 30



Motif II

FIG. 31

